



2121

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/990,415
Source: OPE
Date Processed by STIC: 2/21/2002

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY.**

FOR CRITICAL SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. **EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>), EFS Submission User Manual - ePAVE)**
2. **U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202**
3. **Hand Carry directly to:**
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
Or
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. **Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202**

Raw Sequence Listing Error Summary

<u>ERROR DETECTED</u>	<u>SUGGESTED CORRECTION</u>	<u>SERIAL NUMBER:</u> <u>09/990,415</u>
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 <input checked="" type="checkbox"/> Wrapped Nucleic Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to 3; this will prevent "wrapping."	
2 <input type="checkbox"/> Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 <input type="checkbox"/> Misaligned Amino Numbering	The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.	
4 <input type="checkbox"/> Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 <input type="checkbox"/> Variable Length	Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 <input type="checkbox"/> PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 <input type="checkbox"/> Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (ii) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 <input type="checkbox"/> Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000	
9 <input type="checkbox"/> Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa; and which residue n or Xaa represents.	
10 <input type="checkbox"/> Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence	
11 <input type="checkbox"/> Use of <220>	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 <input type="checkbox"/> PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 <input type="checkbox"/> Misuse of n	n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.	



OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/990,415

DATE: 02/21/2002
TIME: 12:16:35

Input Set : A:\EP.txt
Output Set: N:\CRF3\02212002\I990415.raw

3 <110> APPLICANT: Pharmacia AB
5 <120> TITLE OF INVENTION: Protein Cluster I
7 <130> FILE REFERENCE: 00349
C--> 9 <140> CURRENT APPLICATION NUMBER: US/09/990,415
C--> 9 <141> CURRENT FILING DATE: 2001-11-21
9 <160> NUMBER OF SEQ ID NOS: 8
11 <170> SOFTWARE: PatentIn version 3.0

Does Not Comply
Corrected Diskette Needed

ERRORED SEQUENCES

13 <210> SEQ ID NO: 1
14 <211> LENGTH: 1232
15 <212> TYPE: DNA
16 <213> ORGANISM: human
19 <220> FEATURE:
20 <221> NAME/KEY: CDS
21 <222> LOCATION: (450)..(1232)
24 <400> SEQUENCE: 1
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26 60
E--> 28 accccagttc tggttctgac gccctagctc attccgcaaa tttagggctt gggctctggct
29 120
E--> 31 tggccccctc cggctcgaac cacctttctt ctgagccgag ccagctaccc gggctctgg
32 180
E--> 34 aattgccacc cttccctggg caccctttag gctccgtgg agggacgtca cggggcagag
35 240
E--> 37 cgggacgtga gcctgagttt gctgcaggcg tgctctgtgt ggtggctggg ttctgccaat
38 300
E--> 40 ccccggtgccc accgggtggg cggggccggg aagctcctgc ccctccctgc tggtcggcgt
41 360
E--> 43 cacgcgtgac gtcccgctg atggctggga gggccggcg ggcacagcg aggcaagag
44 420
E--> 46 gaaggcgggtt ctgagagctt cagagacgc atg gaa agc aaa atg ggt gaa ttg
47 473
48 Met Glu Ser Lys Met Gly Glu Leu
49 1 5
E--> 51 cct tta gac atc aac atc cag gaa cct cgc tgg gac caa agt act ttc
52 521
53 Pro Leu Asp Ile Asn Ile Gln Glu Pro Arg Trp Asp Gln Ser Thr Phe
54 10 15 20
E--> 56 ctg ggc aga gcc cgg cac ttt ttc act gtt act gat cct cga aat ctg
57 569

See item 1 on Error Summary sheet
(global)
(format error)

60

120

↓

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PATENT APPLICATION: US/09/990,415

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Input Set : A:\EP.txt
Output Set: N:\CRF3\02212002\I990415.raw

58 Leu Gly Arg Ala Arg His Phe Phe Thr Val Thr Asp Pro Arg Asn Leu
59 25 30 35 40
E--> 61 ctg ctg tcc ggg gca cag ctg gaa gct tct cgg aac atc gtg cag aac
62 617
63 Leu Leu Ser Gly Ala Gln Leu Glu Ala Ser Arg Asn Ile Val Gln Asn
64 45 50 55
E--> 66 tac agg gcc ggc gtg gtg acc cca ggg atc acc gag gac cag ctg tgg
67 665
68 Tyr Arg Ala Gly Val Val Thr Pro Gly Ile Thr Glu Asp Gln Leu Trp
69 60 65 70
E--> 71 agg gcc aag tat gtg tat gac tcc gcc ttc cat ccc gac aca ggg gag
72 713
73 Arg Ala Lys Tyr Val Tyr Asp Ser Ala Phe His Pro Asp Thr Gly Glu
74 75 80 85
E--> 76 aag gtg gtc ctg att ggc cgc atg tca gcc cag gtg ccc atg aac atg
77 761
78 Lys Val Val Leu Ile Gly Arg Met Ser Ala Gln Val Pro Met Asn Met
79 90 95 100
E--> 81 acc atc act ggc tgc atg ctc aca ttc tac agg aag acc cca acc gtg
82 809
83 Thr Ile Thr Gly Cys Met Leu Thr Phe Tyr Arg Lys Thr Pro Thr Val
84 105 110 115 120
E--> 86 gtg ttc tgg cag tgg gtg aat cag tcc ttc aat gcc att gtt aac tac
87 857
88 Val Phe Trp Gln Trp Val Asn Gln Ser Phe Asn Ala Ile Val Asn Tyr
89 125 130 135
E--> 91 tcc aac cgc agt ggt gac act ccc atc act gtg agg cag ctg ggg aca
92 905
93 Ser Asn Arg Ser Gly Asp Thr Pro Ile Thr Val Arg Gln Leu Gly Thr
94 140 145 150
E--> 96 gcc tat gtg agt gcc acc act gga gct gtg gcc acg gcc ctg gga ctc
97 953
98 Ala Tyr Val Ser Ala Thr Thr Gly Ala Val Ala Thr Ala Leu Gly Leu
99 155 160 165
E--> 101 aaa tcc ctc acc aag cac ctg ccc ccc ttg gtc ggc aga ttt gtg ccc
102 1001
103 Lys Ser Leu Thr Lys His Leu Pro Pro Leu Val Gly Arg Phe Val Pro
104 170 175 180
E--> 106 ttt gca gca gtg gca gct gcc aac tgc atc aac atc ccc ctg atg agg
107 1049
108 Phe Ala Ala Val Ala Ala Asn Cys Ile Asn Ile Pro Leu Met Arg
109 185 190 195 200
E--> 111 cag aga gag ctg cag gtg ggc atc ccg gtg gct gat gag gca ggt cag
112 1097
113 Gln Arg Glu Leu Gln Val Gly Ile Pro Val Ala Asp Glu Ala Gly Gln
114 205 210 215
E--> 116 agg ctt ggc tac tcg gtg act gca gcc aag cag gga atc ttc cag gtg
117 1145
118 Arg Leu Gly Tyr Ser Val Thr Ala Ala Lys Gln Gly Ile Phe Gln Val

Patent

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TIME: 12:16:35

Input Set : A:\EP.txt
Output Set: N:\CRF3\02212002\I990415.raw

119 220 225 230
E--> 121 gtg att tca aga atc tgc atg gcg att cct gcc atg gcc atc cca cca
122 1193
123 Val Ile Ser Arg Ile Cys Met Ala Ile Pro Ala Met Ala Ile Pro Pro
124 235 240 245
E--> 126 ctg atc atg gac act ctg gag aag aaa gac ttc ctg aag
127 1232
128 Leu Ile Met Asp Thr Leu Glu Lys Lys Asp Phe Leu Lys
129 250 255 260
190 <210> SEQ ID NO: 3
191 <211> LENGTH: 1061
192 <212> TYPE: DNA
193 <213> ORGANISM: human
195 <220> FEATURE:
196 <221> NAME/KEY: CDS
197 <222> LOCATION: (450)..(680)
199 <400> SEQUENCE: 3
E--> 200 cccttaggcg ccagggacag ccgagcgtta cctggtcccg ggcagcggag ttctttaccc
201 60
E--> 203 acccccagttc tggttctgac gccctagctc attccgcaaa ttttagggctt gggctggct
204 120
E--> 206 tggccccctc cggctcgaac cacctttctt ctgagccgag ccagctacccg gggctcctgg
207 180
E--> 209 aattgccacc cctccctggg caccctttag gcctccgtgg agggacgtca cggggcagag
210 240
E--> 212 cgggacgtga gcctgagttt gctgcaggcg tgctctgtgt ggtggctggg ttctgccaat
213 300
E--> 215 ccccggtgccc accgggtggg cgcggccggg aagctctgc ccctccctgc tggtcggcgt
216 360
E--> 218 cacgcgtgac gtcccgctg atggctggga gggcccgccg ggcacacggg aggccagag
219 420
E--> 221 gaaggcgggtt ctgagagctt cagagagcg atg gaa agc aaa atg ggt gaa ttg
222 473
223 Met Glu Ser Lys Met Gly Glu Leu
224 1 5
E--> 226 cct tta gac atc aac atc cag gaa cct cgc tgg gac caa agt act ttc
227 521
228 Pro Leu Asp Ile Asn Ile Gln Glu Pro Arg Trp Asp Gln Ser Thr Phe
229 10 15 20
E--> 231 ctg ggc aga gcc cgg cac ttt ttc act gtt act gat cct cga aat ctg
232 569
233 Leu Gly Arg Ala Arg His Phe Phe Thr Val Thr Asp Pro Arg Asn Leu
234 25 30 35 40
E--> 236 ctg ctg tcc ggg gca cag ctg gaa gct tct cgg aac atc gtg cag aac
237 617
238 Leu Leu Ser Gly Ala Gln Leu Glu Ala Ser Arg Asn Ile Val Gln Asn
239 45 50 55
E--> 241 tac agg aag acc cca acc gtg gtg ttc tgg cag tgg gtg aat cag tcc
242 665

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Input Set : A:\EP.txt

Output Set: N:\CRF3\02212002\I990415.raw

243 Tyr Arg Lys Thr Pro Thr Val Val Phe Trp Gln Trp Val Asn Gln Ser
 244 60 65 70
 E--> 246 ttc aat gcc att gtt aactactcca accgcagtgg tgacactccc atcactgtga
 247 720
 248 Phe Asn Ala Ile Val
 249 75
 E--> 251 ggcagctggg gacagcctat gtgagtgcca ccactggagc tgtggccacg gccctgggac
 252 780
 E--> 254 tcaaattcct caccaagcac ctgccccct tggcggcag atttgtgcc tttcagcag
 255 840
 E--> 257 tggcagctgc caactgcac aacatcccc tcatgaggca gagagagctg caggtggca
 258 900
 E--> 260 tcccggtggc tcatgaggca ggtcagaggc ttggctactc ggtgactgca gccaagcagg
 261 960
 E--> 263 gaatcttcca ggtggtgatt tcaagaatct gcatggcgat tcctgccatg gccatccac
 264 1020
 E--> 266 cactgatcat ggacactctg gagaagaaag acttcctgaa g
 267 1061
 292 <210> SEQ ID NO: 5
 293 <211> LENGTH: 1567
 294 <212> TYPE: DNA
 295 <213> ORGANISM: human
 297 <220> FEATURE:
 298 <221> NAME/KEY: CDS
 299 <222> LOCATION: (47)..(1015)
 301 <400> SEQUENCE: 5
 E--> 302 gggcatttgt cccgggacca ggtccacagt tttatgttg agcaag atg gag gct
 303 55
 304 Met Glu Ala
 305 1
 E--> 307 gac ctg tct ggc ttt aac atc gat gcc ccc cgt tgg gac cag cgc acc
 308 103
 309 Asp Leu Ser Gly Phe Asn Ile Asp Ala Pro Arg Trp Asp Gln Arg Thr
 310 5 10 15
 E--> 312 ttc ctg ggg aga gtg aag cac ttc cta aac atc acg gac ccc cgc act
 313 151
 314 Phe Leu Gly Arg Val Lys His Phe Leu Asn Ile Thr Asp Pro Arg Thr
 315 20 25 30 35
 E--> 317 gtc ttt gta tct gag cgg gag ctg gac tgg gcc aag gtg atg gtg gag
 318 199
 319 Val Phe Val Ser Glu Arg Glu Leu Asp Trp Ala Lys Val Met Val Glu
 320 40 45 50
 E--> 322 aag agc agg atg ggg gtt gtg ccc cca ggc acc caa gtg gag cag ctg
 323 247
 324 Lys Ser Arg Met Gly Val Val Pro Pro Gly Thr Gln Val Glu Gln Leu
 325 55 60 65
 E--> 327 ctg tat gcc aag aag ctg tat gac tcg gcc ttc cac ccc gac act ggg
 328 295
 329 Leu Tyr Ala Lys Leu Tyr Asp Ser Ala Phe His Pro Asp Thr Gly

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330 70 75 80
E--> 332 gag aag atg aat gtc atc ggg cgc atg tct ttc cag ctt cct ggc ggc
333 343
334 Glu Lys Met Asn Val Ile Gly Arg Met Ser Phe Gln Leu Pro Gly Gly
335 85 90 95
E--> 337 atg atc atc acg ggc ttc atg ctc cag ttc tac agg acg atg ccg gcg
338 391
339 Met Ile Ile Thr Gly Phe Met Leu Gln Phe Tyr Arg Thr Met Pro Ala
340 100 105 110 115
E--> 342 gtg atc ttc tgg cag tgg gtg aac cag tcc ttc aat gcc tta gtc aac
343 439
344 Val Ile Phe Trp Gln Trp Val Asn Gln Ser Phe Asn Ala Leu Val Asn
345 120 125 130
E--> 347 tac acc aac agg aat gcg gct tcc ccc aca tca gtc agg cag atg gcc
348 487
349 Tyr Thr Asn Arg Asn Ala Ala Ser Pro Thr Ser Val Arg Gln Met Ala
350 135 140 145
E--> 352 ctt tcc tac ttc aca gcc aca acc act gct gtg gcc acg gct gtg ggc
353 535
354 Leu Ser Tyr Phe Thr Ala Thr Thr Ala Val Ala Thr Ala Val Gly
355 150 155 160
E--> 357 atg aac atg ttg aca aag aaa gcg ccg ccc ttg gtg ggc cgc tgg gtg
358 583
359 Met Asn Met Leu Thr Lys Lys Ala Pro Pro Leu Val Gly Arg Trp Val
360 165 170 175
E--> 362 ccc ttt gcc gct gtg gct gcg gct aac tgt gtc aat atc ccc atg atg
363 631
364 Pro Phe Ala Ala Val Ala Ala Asn Cys Val Asn Ile Pro Met Met
365 180 185 190 195
E--> 367 cga cag agg gag ctc ata aag gga atc tgc gtg aag gac agg aat gaa
368 679
369 Arg Gln Arg Glu Leu Ile Lys Gly Ile Cys Val Lys Asp Arg Asn Glu
370 200 205 210
E--> 372 aat gag att ggt cat tcc cgg aga gct gcg gcc ata ggc atc acc caa
373 727
374 Asn Glu Ile Gly His Ser Arg Arg Ala Ala Ala Ile Gly Ile Thr Gln
375 215 220 225
E--> 377 gta gtt att tct cgg atc acc atg tca gct cct ggg atg atc ttg ctg
378 775
379 Val Val Ile Ser Arg Ile Thr Met Ser Ala Pro Gly Met Ile Leu Leu
380 230 235 240
E--> 382 cca gtc atc atg gaa agg ctt gag aaa ttg cac ttc atg cag aaa gtc
383 823
384 Pro Val Ile Met Glu Arg Leu Glu Lys Leu His Phe Met Gln Lys Val
385 245 250 255
E--> 387 aag gtc ctg cac gcc cca ttg cag gtc atg ctg agc ggg tgc ttc ctc
388 871
389 Lys Val Leu His Ala Pro Leu Gln Val Met Leu Ser Gly Cys Phe Leu
390 260 265 270 275

Done

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Input Set : A:\EP.txt
Output Set: N:\CRF3\02212002\I990415.raw

E--> 392 atc ttc atg gtg cca gtg gcg tgt ggg ctt ttc cca cag aaa tgt gaa
393 919
394 Ile Phe Met Val Pro Val Ala Cys Gly Leu Phe Pro Gln Lys Cys Glu
395 280 285 290
E--> 397 ttg cca gtt tcc tat ctg gaa ccg aag ctc caa gac act atc aag gcc
398 967
399 Leu Pro Val Ser Tyr Leu Glu Pro Lys Leu Gln Asp Thr Ile Lys Ala
400 295 300 305
E--> 402 aag tat gga gaa ctt gag cct tat gtc tac ttc aat aag ggt ctc taa
403 1015
404 Lys Tyr Gly Glu Leu Glu Pro Tyr Val Tyr Phe Asn Lys Gly Leu
405 310 315 320
E--> 407 atgccccact tcagcaagga ccagtctatt cccatattca ccagtcctc cttagctacg
408 1075 *Parmer*
E--> 410 tgcacacttg tgtcctcctt cccctttgcc aacaaggcct gaaggccagg gtagattgg
411 1135
E--> 413 ggggtgggaca atgaatgcct catacttaca ccctggtaact ggttgattgg acctcagggg
414 1195
E--> 416 aaaaaagtga aaaaggtag caaaggccaa tgtcttctag ctgcttcctc aaccctgtc
417 1255
E--> 419 ccctgagaga ccagaagctg aggcctctc agggaggaga catccaagca aatcatttgg
420 1315
E--> 422 aaaaagtttagg aaaccttttag gattctgggtt ccagccaggg ttgagggaaaa gaccttggat
423 1375
E--> 425 caaaaggaag cttctataacc tctttcttct tcgcttcctc ctctcccaag caatggaaac
426 1435
E--> 428 ttttacccat gtaattctag ctgaactcag gaaaaagaag ggggaaagga ctctgtcccc
429 1495
E--> 431 ttggggctca tcacccttcc acatcctcct cctcgtagcc ccctggtag gcagcttctt
432 1555
E--> 434 tttttttttt tc
435 1567
507 <210> SEQ ID NO: 7
508 <211> LENGTH: 2269
509 <212> TYPE: DNA
510 <213> ORGANISM: human
512 <220> FEATURE:
513 <221> NAME/KEY: CDS
514 <222> LOCATION: (125)..(1093)
516 <220> FEATURE:
517 <221> NAME/KEY: misc_feature
518 <222> LOCATION: (25)..(25)
519 <223> OTHER INFORMATION: n=A,T,G or C
521 <400> SEQUENCE: 7
E--> 522 gacgcgctcc ggggacgcgc gaggncgccg tggcgggaga agcgttccg gtggcggcgg
523 60
E--> 525 aggctgcact gagcgggacc tggcgagcag cgcggcggc agcccgaaaa aagcgtccgg
526 120
E--> 528 gacc atg tct gga gaa cta cca cca aac att aac atc aag gaa cct cga

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Input Set : A:\EP.txt
Output Set: N:\CRF3\02212002\I990415.raw

529 169
530 Met Ser Gly Glu Leu Pro Pro Asn Ile Asn Ile Lys Glu Pro Arg
531 1 5 10 15
E--> 533 tgg gat caa agc act ttc att gga cga gcc aat cat ttc ttc act gta
534 217
535 Trp Asp Gln Ser Thr Phe Ile Gly Arg Ala Asn His Phe Phe Thr Val
536 20 25 30
E--> 538 act gac ccc agg aac att ctg tta acc aac gaa caa ctc gag agt gcg
539 265
540 Thr Asp Pro Arg Asn Ile Leu Leu Thr Asn Glu Gln Leu Glu Ser Ala
541 35 40 45
E--> 543 aga aaa ata gta cat gat tac agg cag gga att gtt cct cct ggt ctt
544 313
545 Arg Lys Ile Val His Asp Tyr Arg Gln Gly Ile Val Pro Pro Gly Leu
546 50 55 60
E--> 548 aca gaa aat gaa ttg tgg aga gca aag tac atc tat gat tca gct ttt
549 361
550 Thr Glu Asn Glu Leu Trp Arg Ala Lys Tyr Ile Tyr Asp Ser Ala Phe
551 65 70 75
E--> 553 cat cct gac act ggt gag aag atg att ttg ata gga aga atg tca gcc
554 409
555 His Pro Asp Thr Gly Glu Lys Met Ile Leu Ile Gly Arg Met Ser Ala
556 80 85 90 95
E--> 558 cag gtt ccc atg aac atg acc atc aca ggt tgt atg atg acg ttt tac
559 457
560 Gln Val Pro Met Asn Met Thr Ile Thr Gly Cys Met Met Thr Phe Tyr
561 100 105 110
E--> 563 agg act acg ccg gct gtg ctg ttc tgg cag tgg att aac cag tcc ttc
564 505
565 Arg Thr Thr Pro Ala Val Leu Phe Trp Gln Trp Ile Asn Gln Ser Phe
566 115 120 125
E--> 568 aat gcc gtc gtc aat tac acc aac aga agt gga gac gca ccc ctc act
569 553
570 Asn Ala Val Val Asn Tyr Thr Asn Arg Ser Gly Asp Ala Pro Leu Thr
571 130 135 140
E--> 573 gtc aat gag ttg gga aca gct tac gtt tct gca aca act ggt gcc gta
574 601
575 Val Asn Glu Leu Gly Thr Ala Tyr Val Ser Ala Thr Thr Gly Ala Val
576 145 150 155
E--> 578 gca aca gct cta gga ctc aat gca ttg acc aag cat gtc tca cca ctg
579 649
580 Ala Thr Ala Leu Gly Leu Asn Ala Leu Thr Lys His Val Ser Pro Leu
581 160 165 170 175
E--> 583 ata gga cgt ttt gtt ccc ttt gct gcc gta gct gct gct aat tgc att
584 697
585 Ile Gly Arg Phe Val Pro Phe Ala Ala Val Ala Ala Asn Cys Ile
586 180 185 190
E--> 588 aat att cca tta atg agg caa agg gaa ctc aaa gtt ggc att ccc gtc
589 745

Parrot

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/990,415

DATE: 02/21/2002
TIME: 12:16:35

Input Set : A:\EP.txt
Output Set: N:\CRF3\02212002\I990415.raw

590 Asn Ile Pro Leu Met Arg Gln Arg Glu Leu Lys Val Gly Ile Pro Val
591 195 200 205
E--> 593 acg gat gag aat ggg aac cgc ttg ggg gag tcg gcg aac gct gcg aaa
594 793
595 Thr Asp Glu Asn Gly Asn Arg Leu Gly Glu Ser Ala Asn Ala Ala Lys
596 210 215 220
E--> 598 caa gcc atc acg caa gtt gtc gtg tcc agg att ctc atg gca gcc cct
599 841
600 Gln Ala Ile Thr Gln Val Val Val Ser Arg Ile Leu Met Ala Ala Pro
601 225 230 235
E--> 603 ggc atg gcc atc cct cca ttc att atg aac act ttg gaa aag aaa gcc
604 889
605 Gly Met Ala Ile Pro Pro Phe Ile Met Asn Thr Leu Glu Lys Lys Ala
606 240 245 250 255
E--> 608 ttt ttg aag agg ttc cca tgg atg agt gca ccc att caa gtt ggg tta
609 937
610 Phe Leu Lys Arg Phe Pro Trp Met Ser Ala Pro Ile Gln Val Gly Leu
611 260 265 270
E--> 613 gtt ggc ttc tgt ttg gtg ttt gct aca ccc ctg tgt tgt gcc ctg ttt
614 985
615 Val Gly Phe Cys Leu Val Phe Ala Thr Pro Leu Cys Cys Ala Leu Phe
616 275 280 285
E--> 618 cct cag aaa agt tcc atg tct gtg aca agc ttg gag gcc gag ttg caa
619 1033
620 Pro Gln Lys Ser Ser Met Ser Val Thr Ser Leu Glu Ala Glu Leu Gln
621 290 295 300
E--> 623 gct aag atc caa gag agc cat cct gaa ttg cga cgc gtg tac ttc aat
624 1081
625 Ala Lys Ile Gln Glu Ser His Pro Glu Leu Arg Arg Val Tyr Phe Asn
626 305 310 315
E--> 628 aag gga ttg taa agcagagagg aaacctctgc agtcattct gccactgcaa
629 1133
630 Lys Gly Leu
631 320
E--> 633 agctgggtgtta gccatgctgg tgagaaaaat cctgttcaac ctgggttctc ccagttacgg
634 1193
E--> 636 aaacctttta aagatccaca ttagcctttt agaataaagc tgctacttta acagagcacc
637 1253
E--> 639 tggcgtgggc caagtgcctg atactccctt acactgaatc atgttatgtat ttatagaaat
640 1313
E--> 642 acctttcctg tagttttat agtcattgtt ttcaaagac gatataccag' ccctcaccca
643 1373
E--> 645 gttttaaaaa aagcactggt aggcataaaaa tagtgctca gtatatggtc agtaaatgtt
646 1433
E--> 648 ctattgatta tcaatcagtg aaaaaagaaa tctgtttaaa atactgaatt ttcatctcac
649 1493
E--> 651 tcccattgca aatcaaggag atctcagcag tgaactggga aaataaaaaa gctctgggct
652 1553
E--> 654 aatctataaa aacttacctg aaatattaag ggcagttgc ttctagttt gggattgcgc

mane

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/990,415

DATE: 02/21/2002
TIME: 12:16:35

Input Set : A:\EP.txt
Output Set: N:\CRF3\02212002\I990415.raw

655 1613
E--> 657 tagcccaatg aagggtatga agctttgga tttggagggt aaaagctcct tcacacccct
658 1673
E--> 660 tccaaaagtc agtcacagac cactgcaaca tgccctccct gctggatcat tatatacatt
661 1733
E--> 663 cagattgtga gtggattgcc ttgggttact tttatattat tgtttttgt tcttataaaag
664 1793
E--> 666 atgataatct taccttgcag ttattgactt tatattcaat tatttacatc aaataatgaa
667 1853
E--> 669 ataactgaaa tgtacaaatg tcaaattttg gaagtatatt caataccaaat gctgtatgag
670 1913
E--> 672 tgggctgaat ccagttcatt gttttttttt tggttagaag tgagactaca gttccagcta
673 1973
E--> 675 cctacatgtc ttttcttgc atccttatacg atcttttgg ctttcagaaa gatacagtga
676 2033
E--> 678 taatgtgtgt atgaatcagt cacaatgaat tttacttgaa tattgtatgt tgcattccac
679 2093
E--> 681 ttcatttgaa aataatgaaa ccatgtacca ctgtttacat catctgtatgt gatttcatag
682 2153
E--> 684 ataatatatt taatatgaca gattatgtt caactctgta gatgttaac gtcatalogaca
685 2213
E--> 687 gtcggccctc tgtatccgtg agctctatat ctgtgaattc aaccaagttt ggatgg
688 2269

part 1

see next page for more error

<210> 8
<211> 322
<212> PRT
<213> human

<220>
<221> misc_feature
<222> (25)..(25)
<223> n=A, T, G or C

<400> 8

"n" is only used in a nucleotide sequence.

This sequence is
a peptide sequence

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/990,415

DATE: 02/21/2002
TIME: 12:16:36

Input Set : A:\EP.txt
Output Set: N:\CRF3\02212002\I990415.raw

L:9 M:270 C: Current Application Number differs, Replaced Current Application No
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:25 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:1
M:254 Repeated in SeqNo=1
L:200 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:3
M:254 Repeated in SeqNo=3
L:302 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:55 SEQ:5
M:254 Repeated in SeqNo=5
L:522 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:522 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:7
M:254 Repeated in SeqNo=7